

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1 1. (Currently Amended) A method for treating HIV infection in a human,
2 wherein HIV entry into an immune cell is facilitated by a CCR5 receptor, said method
3 comprising:
4 a) transplanting into the human a stem cell-rich population of cells from a human
5 donor, wherein the stem cell-rich population of cells has a beneficial gene that is a homozygous
6 polymorphism in a CCR5 gene and the encoded CCR5 receptor does not facilitate HIV entry into
7 the immune cell, wherein in the polymorphism is a 32 basepair deletion in the coding region of
8 the CCR5 gene or a CCR5m303 mutant, and wherein the immune cells of said human are
9 reduced or eliminated prior to transplantation, thereby ~~preventing or~~ treating said HIV infection,
10 wherein HIV entry into the immune cell of said human is facilitated by the CCR5 receptor and
11 wherein the stem cell-rich population of cells is umbilical cord blood.

2-19 (Canceled)

1 20. (Previously presented) The method of claim 1, wherein said method
2 further comprises identification of the HLA genotype or phenotype of said stem cell-rich
3 population of cells.

21-23 (Canceled)

1 24. (Previously presented) The method of claim 1, further comprising a step
2 of screening a cell sample from a human donor to identify the stem cell-rich population of cells
3 that has a polymorphism in the CCR5 gene.

1 25. (Previously presented) The method of claim 24, wherein said
2 polymorphism in the CCR5 gene is detected using a hybridization-based assay, a sequencing
3 assay, or a functional assay.

26-27 (Canceled)

1 28. (Previously presented) The method of claim 24, wherein said method
2 further comprises

3 b) identification of an HLA genotype or phenotype of said stem cell-rich
4 population of cells.

1 29. (Previously presented) The method of claim 28, wherein said
2 identification of the HLA genotype is via a high-throughput method using allele-specific primers
3 and HLA locus-specific capture oligonucleotides immobilized on a solid phase.

1 30. (Previously presented) The method of claim 28, wherein said method
2 further comprises

3 c) identification of an HLA genotype or phenotype of said human.

1 31. (Previously presented) The method of claim 28, wherein said HLA
2 genotype or phenotype of said stem cell-rich population of cells is compatible with said HLA
3 genotype or phenotype of said human.

32. (Canceled)

1 33. (Previously presented) The method of claim 1, wherein multiple samples
2 of the stem cell-rich populations of cells with the beneficial gene are transplanted into the
3 human.

1 34. (Previously presented) The method of claim 33, wherein the multiple
2 samples of the stem cell-rich populations of cells with the beneficial gene have an HLA
3 unmatched genotype or phenotype.